





A;Reference number: A56715; MUID:95279439; PMID:7759551  
A;Accession: A56715  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1078 <GAR>  
A;Cross-references: GB:U20759; NID:G683744; PIDN:AAA86503.1; PID:G683745  
R;Pearce, S.H.S.; Thakker, R.V.  
submitted to the EMBL Data Library, August 1994  
A;Reference number: S49341  
A;Accession: S49341  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-180,'Q',182-989,'R',991-1078 <PEA>  
A;Cross-references: EMBL:X81086  
R;Pollak, M.R.; Brown, E.M.; Chou, Y.H.; Hebert, S.C.; Marx, S.J.; Steinmann, B.; Levi,  
Cell 75, 1297-1303, 1993  
A;Title: Mutations in the human Ca(2+)-sensing receptor gene cause familial hypocalciuric  
A;Reference number: A49419; MUID:94094324; PMID:7916660  
A;Accession: A49419  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 178-192 <POL>  
A;Experimental source: family N  
A;Note: sequence inconsistent with nucleotide translation  
A;Note: sequence modified after extraction from NCBI backbone  
A;Note: 186-Arg mutation is associated with familial hypocalciuric hypercalcemia and nec  
A;Note: sequence extracted from NCBI backbone (NCBIN:142453)  
A;Accession: B49419  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 289-303 <PO2>  
A;Experimental source: family E  
A;Note: sequence modified after extraction from NCBI backbone  
A;Note: 298-Lys mutation is associated with familial hypocalciuric hypercalcemia and nec  
A;Note: sequence extracted from NCBI backbone (NCBIN:142455)  
A;Accession: C49419  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 788-802 <PO3>  
A;Experimental source: family J  
A;Note: sequence modified after extraction from NCBI backbone  
A;Note: 796-Trp mutation is associated with familial hypocalciuric hypercalcemia and nec  
A;Note: sequence extracted from NCBI backbone (NCBIN:142457)  
C;Keywords: glycoprotein; receptor; transmembrane protein

Query Match 34.4%; Score 1687.5; DB 2; Length 1078;  
Best Local Similarity 38.0%; Pred. No. 1.5e-115;  
Matches 353; Conservative 179; Mismatches 333; Indels 63; Gaps 18;

Qy 18 LAFLW--AELGSEAKEEKEERTCRLLGKCVDNAENHSLVIGGLFPIDSRTPANESI-LE 74  
Db 11 LALTWHTSAYGPDQRAQKGD-----IILGGLFPIHFVGAQKQDLKSR 54

Qy 75 PASAKCEGFNFQFRFMKAMIHMIKEINKRKDILPNITLGYQIFDTCFTISKSVEAVLVF 134  
Db 55 PESVECI RYNFRGRWLQAMIFAIEEINSSPALLPNLTIGYRIFDTCNTVSKALEATLSF 114

Qy 135 LTGQE---ENRPNFRNSTGAPPA--GIVGAGGSFSLVSPASRIILGLYLPQVGYTSTCVIL 189  
Db 115 VAQNKIDSLNLDDEFCNCSEHIPSTIAVVGATSGVSTAVANLGLFYIPQVSYASSRLL 174

Qy 190 SDKYQFPFSLRVIASDKIQSKAVVRIQHFGVWVGAIADDDYKGYGVKTFKEKMSAN 249  
Db 175 SNKNQFKSLRTIPNDEHQATAMADIEYFRWNVVGTTIAADDDYGRPGIEKFREAEERD 234

Qy 250 LCVAFSETIPKVSNEKMQKAVKVTSTAKVIVLYTSDILSLFVLEMIHNIITORTWI 309  
Db 235 ICIDFSELLISQYDDEEIQHVVEIQNSTAKVIVWFSSGPDLEBIKEIVRRNITGKIWL 294

Qy 310 ATEAWITSALIAKPEYFPYFGGTIGFATPRSVIPGLKEFLYDVHPNKPNDVLTIEFWOT 369  
Db 295 ASEAWASSSLIAMPQYFHVVGTTIGFALKAGQIPGFRFLKKVHPKSVHNGFAKEFWEE 354

Qy 370 AFNC-TWPNSSVPYNVDHRVNMGTKE---DRLYDMSD---QLCTGEEKLEDLKNYTLDT 422  
Db 355 TFNCHLQEGAKGPLVD--TFLRGHEESGDRFSNSSTAFRPLCTGDENISSVETPYIDYT 412

Qy 423 QLRITKQCKQAVYAIAGLDHLSRCQEGQGGPFGSNQOQCAVIPTDFWQLMYMKEIKFKS 482  
Db 413 HLRISYNYVLAVYSIAHALQDIYTCPLPGRGLF-TNGSCADIKKVEAWQVLKHLRLNFTN 471

Qy 483 HEDKWVILDDNGDLKNGHYDVLNWHLN-DEGEISFVTGGRFNRSTNFEIVPTNSTIFW 541  
Db 472 NMGEQVTFDECDLV-GNYSINWHLSPEDGSIVFKEVGYNYVYAKKGERLFINEEKILW 530

Qy 542 NTESSRLPHSVCTDVCPPGTGRGFVQREPICCFDSIPCADGHVSRKPGERECEQCQGEDY 601  
Db 531 SGFSREVPFNSCSRDCLAGTRKGIIEGEPTCCFECVCECPDEYSDETASACNKCDDDFW 590

Qy 602 SNAQKSECVLKEVEYLAYDEALGFTLVILSVFGAFVVLAVTAVVVIHRHTPLVNASDWQL 661  
Db 591 SNENHTSCIAKEIEFLSWTEPFGLALTFLFAVLGIFLTAFVLGVFIKFRNTPIVKATNREL 650

Qy 662 GFLIQVSLIIMLLSSMLFDKPHNWSMAGQVTLALGFSCLCLSGTSSLFLAYRISK 721  
Db 651 SYLLLFSLCCFSSSLFFIGEPQDWTCLRLQPAFGISFVLCISCLVKTNRVLLVF---E 707

Qy 722 SKTQLTSMHPLYRK-----IIVLISVLAIEIGICTAXLILEPPMVYKNMESQNTKIIL 773  
Db 708 AKIP-TSPH---RKWGLNLQFLLVFLCTFMQIVICVIWLYTAPPSSYRNQOLEDEIIFI 763

Qy 774 GCNEISIEFLYSMEGIDAFIALLCFLTTFVARQLPDNYYGKCIITFGMLVFFIWMFVP 833  
Db 764 TCHESLMALGFLIGYTCLLAAICFFFAFKSRKLPENFNEAKPITFSMLIFFIVWISFIP 823

Qy 834 VYLSTGKFKMAVEIFAILASSHGLGCI FAPKCLIIILLRPERNTSEIVCGRVSTTDCNCI 893  
Db 824 AYASTYGKFVSAVEVIAILAAASFGLLACIFFNKIYIILFKPSRNTIEEV--RCSTAAHAF 881

Qy 894 QLTSAPV-----SSELNNTTVST 911  
Db 882 KVAARATLRRSNVSRKRSSSLGGSTGST 909

RESULT 4  
B56715  
calcium receptor (clone pHpCaR-5.2) - human  
C;Species: Homo sapiens (man)  
C;Date: 19-Oct-1995 #sequence\_revision 19-Oct-1995 #text\_change 21-Jul-2000  
C;Accession: B56715  
R;Garrett, J.E.; Capuano, I.V.; Hammerland, L.G.; Hung, B.C.P.; Brown, E.M.; Hebert, S.  
J. Biol. Chem. 270, 12919-12925, 1995  
A;Title: Molecular cloning and functional expression of human parathyroid calcium receptor  
A;Reference number: A56715; MUID:95279439; PMID:7759551  
A;Accession: B56715  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-1088 <GAR>  
A;Cross-references: GB:U20760; NID:G683746; PIDN:AAA86504.1; PID:G683747  
C;Keywords: glycoprotein; receptor; transmembrane protein

Query Match 34.1%; Score 1673.5; DB 2; Length 1088;  
Best Local Similarity 37.6%; Pred. No. 1.6e-114;  
Matches 353; Conservative 180; Mismatches 332; Indels 73; Gaps 19;

Qy 18 LAFLW--AELGSEAKEEKEERTCRLLGKCVDNAENHSLVIGGLFPIDSRTPANESI-LE 74  
Db 11 LALTWHTSAYGPDQRAQKGD-----IILGGLFPIHFVGAQKQDLKSR 54

Qy 75 PASAKCEGFNFQFRFMKAMIHMIKEINKRKDILPNITLGYQIFDTCFTISKSVEAVLVF 134  
Db 55 PESVECI RYNFRGRWLQAMIFAIEEINSSPALLPNLTIGYRIFDTCNTVSKALEATLSF 114

Qy 135 LTGQE---ENRPNFRNSTGAPPA--GIVGAGGSFSLVSPASRIILGLYLPQVGYTSTCVIL 189  
Db 115 VAQNKIDSLNLDDEFCNCSEHIPSTIAVVGATSGVSTAVANLGLFYIPQVSYASSRLL 174



QY 190 SDKYQFPSYLRVIAADKIQSKAVVVKRIQHFGVWVGAIADDDYGYGVKTFKEMESAN 249  
Db 175 SNKQKFSFLRTIPNDEHQATAMADIIEYFRWNWGTIAADDDYGRPGIEKPREAEERD 234  
QY 250 LCVAFSETIPKVSNEKQKAVKAVKTSTAKVIVLYTSDIDLSLFVLEMIHNTDRTWI 309  
Db 235 ICIDFSELISQYDEBEIQHVVVEIQNSTAKVIVFSSGPDLEPLIKEIVRRNITGKIWL 294  
QY 310 ATEAWITSAIAKPEYFPYFGGTIGFATPRSVIPGLKEFLYDVHPNKPNDVLTIEFWOT 369  
Db 295 ASEAWASSSLIAMPQYFHVVGTTIGFALKAGQIPGPREFLKKVHPKSVHNGFAKEFWEE 354  
QY 370 AFNC-TWPNSSVPYNVDHRVNMVTKG---DRLYDMSD---QLCTGEEKLEDLKNLYLDT 422  
Db 355 TFNCHLQEGAKGLPVD--TFLRGHEESGDRFNSSTAERPLCTGDNISSETPYIDYT 412  
QY 423 QLRTKQCKQAVYAIAGHLDHLSRCQEGQGFSGNQCCAYIPTDFWQLMYMKEIKFES 482  
Db 413 HLRISYNNVYLAIVSYIAHALQDIYTCLPGRGLF-TNGSCADIKKVEAWQVKKHLRLNFTN 471  
QY 483 HEDKWVILDDNGDLKNGHYDVNLNHL-DGEISFTVTVGRFNRFRSTNFEVLPIPTNSTIFW 541  
Db 472 NMGEQVTFDECGDLV-GNYSIINWHLSPEDGSIVFKEVGYNNVYAKKGERLFINEEKILW 530  
QY 542 NTESS-----RLPHSVCTDVCPPGTGRGFVQREPICCFDSIPCADGHVSRKPGER 591  
Db 531 SGFSREPLTFVLSVLQVFPFNSCRDCLAGTRKGIIEGETCCFECVCEPDGEYSDETDAS 590  
QY 592 ECQCGEDYWSNAQSECVLKEVEYLAYDEALGFTLVLSVFGAFVVLAVTAVYVIHRHT 651  
Db 591 ACNKPDDFWNSNENHTSCIAKEIEFLSWTEPFGIALTLFAVLGIFLTAFLVGVFIKFRNT 650  
QY 652 PLVNASDWQLGFLIQVSLIIMLLSSMLFIDKPHNWSMAGQVTLALGFSCLSLGKTS 711  
Db 651 PIVKATNRELSYLLFSLCCFSSSLFFIGBPQDWTCRLRQPAFGISFVLICISILVKTN 710  
QY 712 SLFLAYRISKSTQLTSMHPLYRK-----IIVLSVLAIEIGICTAYLILEPPMVYKN 763  
Db 711 RVLLVF---EAKIP-TSFH---RKWGLNLQFLVFLCTFMQIVICVIWLYTAPPSYRN 763  
QY 764 MESQNTKIILGCNEISIEFLYSMFGIDAFLLALCFLTTFVARQLPDNYYEGKICITFGLV 823  
Db 764 QELEDEIIFITCHEGSLMALGFLIGYTCLLAACFFFAFKSRKLPENFNEAKFITFSMLI 823  
QY 824 FFIWMSFVPVYLSLTKGFKMAVEIFAILASSHGLLGCIFAPKCLIIILRPERNTSEIVC 883  
Db 824 FFIWISFIPAYASTYGFVSASVEVIALAASFGLLACIFFNKIYIILFKPSRNTIEEV- 882  
QY 884 GRVSTTDCIQLTSAFV-----SSELNNTTVST 911  
Db 883 -RCSTAAHAFKVAARATLRRSNVSRKRSSSLGGSTGST 919  
RESULT 5  
JC7683  
taste receptor T1r3 - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 09-Jul-2004  
C;Accession: JC7683  
R;Kitagawa, M.; Kusakabe, Y.; Miura, H.; Ninomiya, Y.; Hino, A.  
Biochem. Biophys. Res. Commun. 283, 236-242, 2001  
A;Title: Molecular genetic identification of a candidate receptor gene for sweet taste.  
A;Reference number: JC7683; MUID:21222875; PMID:11322794  
A;Contents: tongue  
A;Accession: JC7683  
A;Molecule type: mRNA  
A;Residues: 1-858 <KIT>  
A;Cross-references: UNIPROT:Q91VA4; DDBJ:AB049994  
C;Comment: This protein, a seven-transmembrane receptor, serves as a mediator of the sig  
C;Genetics:  
A;Gene: tlr3  
A;Map position: 4

C;Superfamily: metabotropic glutamate receptor 4  
C;Keywords: transmembrane protein  
Query Match 17.2%; Score 845; DB 2; Length 858;  
Best Local Similarity 28.0%; Pred. No. 8.8e-54;  
Matches 238; Conservative 164; Mismatches 382; Indels 66; Gaps 23;  
QY 54 VIGGLFPIDSRITIPANESILEPASAKCEGFNFQFRWMKAMIHMIKEINKRKDILPNITL 113  
Db 36 ILGLFPLGSTTEATLNQRTQNSIPCNRFSPGLGLFLAMAMKMAVEEINNNGSALLPGLRL 95  
QY 114 GYQIFDTCFTISKVSAVLVLTG-QEENRPNFRNSTGAPP--AGIVGAGGSFSLVSPASR 170  
Db 96 GYDLFDTCSEPVVTMKSSLMFLAKVGSQSIAYCNYTQYQPRVLAVIGPHSSELALITGK 155  
QY 171 ILGLYLPQVGYTSTCVILSDKYQFPSPYLRVIAADKIQSKAVVVKRIQHFGVWVGAIAD 230  
Db 156 FFSFELMPQVSYSSASMDRLSDRETFFSFRTVPVSDRVQLQAVVTLNQNFSSWNVVAALGSD 215  
QY 231 DDYKGYGVKTFFKEMESANLCAVAFSETIPKVSNN---EKMOKAVKAVKTSTAKVIVLYT 286  
Db 216 DDYGREGLSIFSSLANARGICIAHEGLVPQHDTSQQLGKVLDRVLRQVNSKVQVWVLF 275  
QY 287 SDIDLSLFVLEMIHNTDRTWIATEAWITSAIAKPEYFPYFGGTIGFATPRSVIPGLK 346  
Db 276 SARAVYSLFSYSIHGLSPKVVVASESWLTSDLVMTLPNTARVGTVLGFLQGALLP--- 332  
QY 347 EFLYDVHPN---KDPNDVLTIEFWQTAFCNTWPNSSVPYNVDHRVNMVTKEDRLYD--M 400  
Db 333 EFSHYVETHLALADP-----AF-C---ASLNAELDLSEHVMGQRCPRCDDIM 376  
QY 401 SDQLCTGEEKLEDLKNLYLDTSQLRITKQCKQAVYAIAGHLDHLSRCQEGQGFSGNQCC 460  
Db 377 LQNLSSG--LLQNLGAGQLH-HQIFAT---YAAVYSVAQALHNTLQCNVSHCHVSEH--- 427  
QY 461 AYIPTDFWQLMYMKEIKPKSHEDKWVILDDNGDLKNGHYDVNLNHLDDGEISFTVTVG 520  
Db 428 -VLP---WQLLENMYNMSFHA-RDLTLQFDAEGNV-DMEYDLKMWVWQSPTPV-LHTVG 479  
QY 521 RNFNRSTNFEVLPIPTNSTIFWNTESRLPHSVCTDVCPPGTGR---GFVQREPICCFDSI 577  
Db 480 TFN---GTLQL---QOSKMYW--PGNQVPVSQCSRQCKDQVRRVKGFHS---CCYDCV 527  
QY 578 PCADGHVSRKPGERECEQGEDYWSNAQSECVLKEVEYLAYDEALGFTLVLSVFGAFV 637  
Db 528 DCKAGSYRKHPDDFTCTPCNQDQWSPEKSTACLPFRPKFLAWGEPVWLSLLLLCLVLGL 587  
QY 638 VLAVTAVYVIHRHTPLVNASDWQLGFLIQVSLIIMLLSSMLFIDKPHNWSMAGQVTLAL 697  
Db 588 ALAALGLSVHHWDSPLVQASGSGFCFGLICLGLFCLSVLFPGRPSSASCLAQOPMAHL 647  
QY 698 GFSCLCLSLGKTSLSFLAYR--ISKSTQLTSMHPLYRKIIIVLSVLAIEIGICTAYLIL 755  
Db 648 PLTGCLSTLFLQAAETFESELPVSWANWLCVLRGLWAWLVLLATFVEAALCAWYLIA 707  
QY 756 EPPMVYKNMESQNTKIILGCNEISIEFLYSMFGIDAFLLALCFLTTFVARQLPDNYYEGK 815  
Db 708 FPPEVTTDWSVLPTEVLEHCHVRSWVSLGLVHITNAMLAFCLGTLGTLVQSOPGRYNR 767  
QY 816 CITFGMLVFFIWMSPVYVYSTKGKFKMAVEIFAILASSHGLLGCIFAPKCLIIILRPE 875  
Db 768 GLTFAMLAYFITWVSFVPLLANVQVAYQPAVQMGAILVCALGILVTFHLPKCYVLLWLPK 827  
QY 876 RNTSEIVCGR 885  
Db 828 LNTQEFFLGR 837  
RESULT 6  
JC7160  
metabotropic glutamate receptor subtype 3 precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 04-Mar-2000 #sequence\_revision 04-Mar-2000 #text\_change 11-May-2000



Db	339	GYEQEAVGG-ITVKLHSEEVTSFDDYFLKLRNLNTNTRNPWFPEFWQHRFQCRIPEGHPLE-	396
Qy	383	NVDHRVNTGKEDRLYDMSDQLCTGEEKLEDLKNLYLDTSQLRITKQCKQAVYAIAGHLD	442
Db	397	NNYRKNN-----CSGYESLED---NYVQDSKMGFV---INAIYAMAQGLH	435
Qy	443	--HLSRCQEGQGPFGSNQQCAYIPTDFWQLMYMKEIKFK--SHEDKWVILDDNGDLKN	498
Db	436	DMHSHLCP-----GHVGLCKAMPIDGSQLLEFLMRTSFTGVSGEDVW--FDENGDTP-	486
Qy	499	GHYDVNLNWHLDDEGEISFVTVGRFNRSTNFELVPIPTNSTIFWNTESSRLPHSVCTDVCP	558
Db	487	GRYEIMNLQYVEPGAFDYINVGSWHEGQLSID-----DYMQINRSDMVLVSCSEPCS	539
Qy	559	PTGRGFVQREPICCFDSIPCADGHVSRKPGERECEQCAGEDYWSNAQKSECVLKEVEYLA	618
Db	540	KGEIKVIRKGEVSCWCWICTACKNEIVQ--DEFTCTACDLGWPDPELEGCEPITRLYLE	597
Qy	619	YDEALGFTLVILSVFGAFVVLAVTAVYVIHRHTPLVNASDWQLGFLIQVSLIIMLLSSML	678
Db	598	WGNPESIVQVVFACLGILVTSFVTFFVLYRDTVPVKSSSRELVCYIILAGIFLGYICPPT	657
Qy	679	FIDKPHNWSMAGQVTLALGFSCLSLGKTSSLFLAYRISKSTQLTSMHPLY-----	733
Db	658	LIAOPTVASCYLQRLVLGLSATMCYSALVTKTNR--IARILAGSKKICKTRKPRFMSAWA	715
Qy	734	RKIIVLISVLAIEIGICTAYLILEPPMVYKMWESQNTKIILGCNEISIEFLYSFMFGIDAF	793
Db	716	QLVIAGLLVSVQLTLEVTLIILEPPMPVKSPSIR-EVFLICNTSTVG-MVAPLGYNGLL	773
Qy	794	ALLCFLTTFVARQLPDNYVEGKCITFGMLVFFIIMWSFVPVYLSKKGKFKMAVEIFA	853
Db	774	IMSCYYAFKTRNVNPAFNEAKYIAFTWYTCIIWLAFAVPIYFGS--NYKIIITTSFSVSL	831
Qy	854	SSHGLGCI FAPKCLIIILLRPERN-----TSEIV-----CGRVSTTDNCI	893
Db	832	SVTVALGCMFSPKIVIIILAKPERNVRSFTTSDVVRMHVGDGNVACRSNSL	882
RESULT 8			
JH0562			
metabotropic glutamate receptor 3 precursor - rat			
C;Species: Rattus norvegicus (Norway rat)			
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004			
C;Accession: JH0562			
R;Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.			
Neuron 8, 169-179, 1992			
A;Title: A family of metabotropic glutamate receptors.			
A;Reference number: JH0561; MUID:92110002; PMID:1309649			
A;Accession: JH0562			
A;Molecule type: mRNA			
A;Residues: 1-879 <TAN>			
A;Cross-references: UNIPROT:P31422			
A;Experimental source: brain			
C;Comment: This protein is coupled to a G protein and evokes a variety of functions by m			
C;Superfamily: metabotropic glutamate receptor 4			
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane pro			
F;1-22/Domain: signal sequence #status predicted <SIG>			
F;23-879/product: metabotropic glutamate receptor 3 #status predicted <MET>			
F;577-599/Domain: transmembrane #status predicted <TRI>			
F;614-634/Domain: transmembrane #status predicted <TII>			
F;646-664/Domain: transmembrane #status predicted <III>			
F;689-709/Domain: transmembrane #status predicted <TIV>			
F;735-756/Domain: transmembrane #status predicted <TRV>			
F;770-791/Domain: transmembrane #status predicted <TVI>			
F;804-828/Domain: transmembrane #status predicted <VII>			
F;209,292,414,439/Binding site: carbohydrate (Asn) (covalent) #status predicted			
F;610,845/Binding site: phosphate (Ser) (covalent) #status predicted			
Query Match 16.6%; Score 814.5; DB 2; Length 879;			
Best Local Similarity 26.6%; Pred. No. 1.6e-51;			
Matches 240; Conservative 166; Mismatches 393; Indels 103; Gaps 30;			

Qy	53	LVIGGLFPIDSRIPANESILEPASAKCEGFNQR-FRWMKAMIMHIKEINKRKDILPNI	111
Db	39	LVLGGLFPINEKGTGTEE-----CGRINEDRGIRLEAMLFAIDEINKDNYLLPGV	89
Qy	112	TLGYQIFDTC----FTISKSVEAVLVFLTGQENRPNFRNSTGAPP-----AGIVG	158
Db	90	KLGVHILDTCSRDTYALEQSLEFVRASLTQVDE--AECMPDGSYAIQENIPLLIAGVIG	147
Qy	159	AGGSFLSVPASRILGLYVLPQVGYTSTCVILSDKYQFPSPYLRVIASDKIQSKAVVKRIQH	218
Db	148	GSYSSVSIQVANLLRLFIQIPQISYASTSAKLSDKSRDYDFARTVPPDFYQAKAMAEILRF	207
Qy	219	FGWVVGAIADDDYKYGKVTFFKEKMEANLQVAFSETIPKVSNEKMQKAVK-AVKTS	277
Db	208	FNWTVSTVASEGDYGETGIEAFEQEARLRNICIATAEKVGRSNIRKSYDSVIRELLQKP	267
Qy	278	TAKVIVLYTSDIDLFLVLEMIHNIITDRTWIAEAWITSALIAK-PEYFPYFGGTIGFA	336
Db	268	NARVVVLFMRSD-SRELIAAANRVNASFTTWASDQWGAQESIVKGEHVAY--GAITLE	324
Qy	337	TPRSVIPGLKEFLVDVHPNKDPNDVLTIEFWQTAFNCTWPNSSVPYNVDRHVNMTGKEDR	396
Db	325	LASHPVQRQDRYFQSLNPNYNNHRNPWFDRFWEQEQCSLQNK-----NHR-----	370
Qy	397	LYDMSDQLCTGEEKLEDLKNLYLDTSQLRITKQCKQAVYAIAGHLDHLSR--COEQGQPF	454
Db	371	-----QVC--DKHLAIDSSNYEQESKIMFV---VNAVYAMAHALHKMORTLCP-----	413
Qy	455	GSNQCCAYIPTDFWQL-MYMKKEIKF-----KSHEDKWVILDDNDGLKNGHYDVLNWH	507
Db	414	NTTKLCDAMKILDGKKLYKEYLLKINFAPFNPNKGADSIKVFDTFGD-GMGRYNVFNQ	472
Qy	508	LDDEGEISFVTVGRFNRSTNFELVPIPTNSTIFWNTESSRLPHSVCTDVCPPTGTRGFVQ	567
Db	473	-QTGGKYSYLVKGVHW-----AETLSLDVDSIHWSRNS--VPTSQSDPCAPNEMKN-MQ	522
Qy	568	REPICCFDSIPCADGHVSRKP-----GERECEQCAGEDYWSNAQKSECVLKEVEYLADEA	622
Db	523	PGDVCCWICIPC-----BPEYELVDEFTCMDCGPGQWFTADLSGCYNLPEDIKWEDA	575
Qy	623	LGFTLVILSVFGAFVVLAVTAVYVIHRHTPLVNASDWQLGFLIQVSLIIMLLSSMLFIDK	682
Db	576	WAIGPVTIACLGFLCTCIVTFIKHNNTPLVKASGRELCYILLFGVSLSYCMTFFFIK	635
Qy	683	PHNWSMAGQVTLALGFSCLSLGKTSSLFLAYRISKSTQLTS-MHPLYRKIIIVLIS	741
Db	636	PSPVICALRRRLGLGTSFAICYSAALLTKTNCIARIFDGVKXGAQRPKFISSQVFCILGL	695
Qy	742	VLABIGICTAYLILEPPMV--YKNMESQNTKIILGCNEISIEFLYSFMFGIDAFLLCFL	799
Db	696	ILVQIVMVSVWLILETPGTRRYTLPEKRET-VILKCNKVDSSMLISL-TYDVVLVILCTV	753
Qy	800	TTFVARQLPDNYEGKCITFGMLVFFIIMWSFVPVYLSKKGKFKMAVEIFAIIASSHG--	857
Db	754	YAFKTRKCPENFNEAKFIGFTMYTTCIIWLAFLPIFYVTSSDYRVQTTWCISVLSGFV	813
Qy	858	LLGCIFAPKCLIIILLRPERNTSEIVCGRVSTTDNCIQLTSAFVSSELNNTTVSTVLD	917
Db	814	VLGCLFAPKQVHIVLFQPKN---VVTHRLHLNRFVSVSGTATTYSQSSASTYVPTVCNGRE	870
Qy	918	LI 919	
Db	871	VL 872	
RESULT 9			
JC2132			
metabotropic glutamate receptor 5 A - human			
C;Species: Homo sapiens (man)			
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996			
C;Accession: JC2132			
R;Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.			
Biochem. Biophys. Res. Commun. 199, 1136-1143, 1994			









QY	158	GAGSFLSV	PASRILGL	YLPQVGYT	STCVILSD	KYQFP	SYLRVIA	SDKIQSKA	VVWKRIQ	217
Db	147	GPSSVAIQ	VQNLLQL	FNIPQIA	YSATSM	DLSDKTL	FKYFMR	VVPSDAQ	QARAMVDIVK	206
QY	218	HFGVWVGA	IAADDDY	KYGVKTF	KEKME	SANLCVAF	SETIPK	VYSN----	ITSALIAKPEYP	326
Db	207	RYNWTYVS	AVHTEG	NYGESG	MEAFK	DMSAKEG	ICIAHSY	--KIYSNAGE	QSPDKLLKGL	263
QY	275	KT--STAK	VIVLYT	SDIDL	SLFVLE	MIHNIT	-DRTWIA	TEAW----	ITSALIAKPEYP	326
Db	264	RSHPKAR	VVACFCE	GTMVTR	GLLMAM	RRGLAGE	FFLLG	SDGWAD	RYDVTDG-----	315
QY	327	PYFGTIG	ATPRSVI	PGLK--	-EFLYD	VHPNKP	DNDVLT	IEFWQTA	FNCNCTWPNSSVPYN	383
Db	316	-YQREAV	GGITIKL	QSPDV	KWFFDD	YVYKL	RPETNL	RNPWFQ	EFWQHRPQC-----	364
QY	384	VDHRVNM	TGKEDRL	YD--MSD	QLCTG	BEKLED	LKNYLD	TSQLRIT	KQCKQAVYIAHGL	441
Db	365	---RL	EGFAQEN	SKYNTC	NSSLTR	THHVQ	DSKMGFV	-----	INAIYSMAYGL	410
QY	442	DH--LSR	CQEGQGP	FGSNQ	QCAIPT	PDFWQ	LMYMK	EIKFKSH	EDKWVILDDNGDLKNG	499
Db	411	HNMQSL	CP-----	GYAGL	CDAMK	PIDGR	KLLDSL	MKTNFT	GVSGDMILFDENG	-SPG 463
QY	500	HYDVLN	WHLLD	DEGEIS	FVTVGR	FNFRST	NFELV	IPNTSTI	FWNTBESSRLPHSVCTDVCPP	559
Db	464	RYEIMNF	KEMGKDY	FYINV	GSWD---	NGELK	MDDEV	--W-SKKN	IIRSVCSSEPCEK	516
QY	560	GTCRGF	VQREPI	CCFDSI	PCADG	HVSRK	PGERECE	QCGEDY	WSNAQKSECVLKEVEYLAY	619
Db	517	GQIKVIR	KGEVSC	CTPCKE	NEYVF-	DEYTKA	CQLGS	WPTDDL	TGCDLIPVQYLRW	574
QY	620	DEALGFT	LVLILS	VFGAF	VVLAVT	AVYVIR	HRTPL	VNASD	WQLGFLIQVSLIMLLSSMLF	679
Db	575	GDPEIAA	WVACLGL	LATLV	TVTFI	YIRDT	PWKSS	SSREL	CIILAGICLGYLCTFCL	634
QY	680	IDKPHN	WSCMAG	QVTLA	LGSLCL	SLGKT	SSLFL	AYRISK	SKTQLTSMHPLY-----R	734
Db	635	IAPKQI	YCYLQ	RIGIGL	SPAM	SYSALV	TKNTR--	IARILAG	SKKICTKKPRFMSACAQ	692
QY	735	KIIVLS	VLAIEG	ICTAYL	ILEP	PMVVK	NMESQ	NTKIIL	GCNEISIEFLYSMF	GIDAFLA 794
Db	693	LVIAFIL	ICIQ	LIIIV	ALFIME	PPDINH	DYPSIR	-EVYLI	CNTTNLG-VVTPLGYNGLLI	750
QY	795	LLCFLT	TFVARQ	LPDN	YEGKCI	TFGML	VFFI	WMSF	VPVYLSTKGFKNVAEIPAILAS	854
Db	751	LSCTFY	AFKTRN	VPAN	FNEAKY	IAFTMY	TTCLII	WLAF	VPYIPGSG--NYKIITMCF	SVSLS 808
QY	855	SHGLL	GCIFAP	KCLII	LLRPER	N-----	TSEIV	882		
Db	809	ATVALG	CMFVPK	VYII	LAKPER	NVRS	AF	TTSTVW	842	

RESULT 13

JH0561

metabotropic glutamate receptor 2 precursor - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004

C/Accession: JH0561

R/Tanabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.  
Neuron 8, 169-179, 1992

A/Title: A family of metabotropic glutamate receptors.

A/Reference number: JH0561; MUID:92110002; PMID:1309649

A/Accession: JH0561

A/Molecule type: mRNA

A/Residues: 1-872 <TAN>

A/Cross-references: UNIPROT:P31421

A/Experimental source: brain

C/Comment: This protein is coupled to a G protein and evokes a variety of functions by m

C/Superfamily: metabotropic glutamate receptor 4

C/Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot

F/1-18/Domain: signal sequence #status predicted <SIG>

F/19-872/Product: metabotropic glutamate receptor 2 #status predicted <MET>

F;568-590/Domain: transmembrane #status predicted <TRI>  
F;605-625/Domain: transmembrane #status predicted <TII>  
F;637-655/Domain: transmembrane #status predicted <TII>  
F;680-700/Domain: transmembrane #status predicted <TV>  
F;726-747/Domain: transmembrane #status predicted <TRV>  
F;761-782/Domain: transmembrane #status predicted <TVI>  
F;795-819/Domain: transmembrane #status predicted <VII>  
F;203,286,338,402,547/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F;601,675,827,837,843/Binding site: phosphate (Ser) (covalent) #status predicted  
F;832/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match	15.6%;	Score 764;	DB 2;	Length 872;
Best Local Similarity	25.3%;	Pred. No. 8.1e-48;		
Matches 240;	Conservative 169;	Mismatches 402;	Indels 136;	Gaps 31;

QY	18	LAPLWABLGSEAKKEEKEERTCRLLGKCVDAENHSLVIGGLFPIDSRITIPANESILEPAS	77
Db	10	LLLLWG-----AVAEGPAKKVLTLEG-----DLVLGGLFPVHQKGPAEE-----	49
QY	78	AKCEGFNFQR-FRWMKAMIHIKEINKRKDILPNITILGYQIFDTCFTTISKSVEAVLVFL-	135
Db	50	--CGPVNEHRGIIORLEAMLFALDRINRDPHLLPGVRLGAHILDCSKDTHALEQALDFVR	107
QY	136	----TGQENR---PNFRNSTGA-PPAGIVGA-GGSF--LSVPASRIILGLYYLPQVGYTS	184
Db	108	ASLSRGADGSRHICPDGSYATHSDAPTAVTGVIGGSYSDVSIQVANLLRLFIQIPQISYAS	167
QY	185	TCVILSDKYQFPSYLRVIASDKIQSKAVVKRIQHFGWVWVGAIADDDYKGKYGVKTFKEK	244
Db	168	TSAKLSDKSRYDYFARTVPPDPFQAKAMAEILRPFNWTYVSTVASEGDYGETGIEAFELE	227
QY	245	MESANLCVAFSETIPKVSNEKMQKAVKA-VKTSTAKVIVLYTSDILSLFVLEMIHNI	303
Db	228	ARARNICVATSEKVGGRAMSRAAFEGVVRALLQKPSARVAVLFTRSEHARELLAATQRLN-	286
QY	304	TDRTWIATEAW-ITSALIAKDEYFPYFGGTIGFATPRSVIPGLKEFLYDVHPNKDPNDVL	362
Db	287	ASFTWVASDVGWGALESVVAGSERAEGAITIELAS--YPISDPASVFSQSLDPWNNSRNPW	344
QY	363	TIEFWQTAFNCTWPN-----SSVPYNVDHRVNMTKEDRLYDMSDQLCTGEEKLEDL	414
Db	345	FREFWEERFHCSFRORDCAHSLRAVPFQESKIMFV-----	381
QY	415	KNTYLDTSQLRITKQCKQAVYAIAGLDHLR--CQ-----EGQGPFSGNQCCAYIPTF	466
Db	382	-----VNAVYAMAHALHNMHRALCPNTHLCDAMRPVNGRR-----	417
QY	467	DPWQLMY--YMKEIKF-----KSHEDKWVILDNDGDLKNGHYDVLNWHLDDEGEISFVTV	519
Db	418	-----LYKDFVLNVKFDAPREFADTDDEVRFDRFGD-GIGRYNIFYLVRAGSGRYRYQKV	471
QY	520	GRFNRSTNPELVIPTNSTIFWNTESS-RLPHSVCTDVCPPGTGRGFVQREPICCFDSIP	578
Db	472	GYW-----AEGTLTDSFIPWASPSAGPLPASRCSEPCQLONEVKS-VQPEGVCCWLCP	524
QY	579	CADGHVSRKPGERECEQGEDYWSNAQKSECVLKEVEYLAYDEALGFTLVILSVFGAFVW	638
Db	525	CQP--YEYRLDEFTCADCGLGYPWNASLTGCFELPQEIYIRWGDAWAGVPVTIACLGALAT	582
QY	639	LAVTAVYVIHRHTPLVNASDWOLGFLIQVSLIIMLLSSMLFIDKPHNWSMCAQVVTLAG	698
Db	583	LPVLGVFVRHNATPVVKASGRELCYILGGVFLCYCMTFVFIKSTAVCTLRRIGLGT	642
QY	699	PSLCLSLGLKGTSSLFLAYRISKSTQLT-S-MHPLYRKIIIVLISVLAIEIGICTAYLILEP	757
Db	643	FSVCYSALLTKTNRIARIFGGAREGAQRPRFISPASQVAICLALISGQLLIIVAAWLVEA	702
QY	758	PMVYKNMESQNTKII-LGCNEISIEFLYSMFGIDAFLLCLFTTFVARQLPDNYEGKC	816
Db	703	PGTGKETAPERREVVTLRCNHRDASMLGSL-AYNVLLIALCTLYAFKTRKCPENFEAKF	761
QY	817	ITFGMLVFFIIWMSFVPVYLSTKGKFKMAVEIFAIIASSHG--LLGCTIPAPKCLIIILRP	874

Db 762 IGFTMYTTCIIWLAFPLIFVYTSSDYRVQTTMCVSVLSGSVVLGCLFAPKLIILFQP 821

QY 875 ERNTSEIVCGRVSTT--DNCIQLTSAFVSSELNNTTVSTVLDDRVL 919

Db 822 QKN---VVSHRAPTSRFGSAAPRASANLQSGSGQFVPTVCNGREV 865

RESULT 14

A49874

metabotropic glutamate receptor 7 - rat

N;Alternate names: metabotropic glutamate receptor mGluR7

C;Species: Rattus norvegicus (Norway rat)

C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004

C;Accession: A49874; I57954

R;Okamoto, N.; Hori, S.; Akazawa, C.; Hayashi, Y.; Shigemoto, R.; Mizuno, N.; Nakanishi, J. Biol. Chem. 269, 1231-1236, 1994

A;Title: Molecular characterization of a new metabotropic glutamate receptor mGluR7 coup

A;Reference number: A49874; MUID:94117433; PMID:8288585

A;Accession: A49874

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-915 <RE>

A;Cross-references: UNIPROT:P35400; GB:D16817; NID:G458728; PIDN:BAA04092.1; PID:G458729

R;Saugstad, J.A.; Kinzie, J.M.; Mulvihill, E.R.; Segerson, T.P.; Westbrook, G.L. Mol. Pharmacol. 45, 367-372, 1994

A;Title: Cloning and expression of a new member of the L-2-amino-4-phosphonobutyric acid

A;Reference number: I57954; MUID:94195260; PMID:8145723

A;Accession: I57954

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-915 <RE2>

A;Cross-references: EMBL:U06832; NID:G459657; PIDN:AAA20655.1; PID:G459658

C;Genetics:

A;Gene: MGLUR7

C;Superfamily: metabotropic glutamate receptor 4

C;Keywords: neurotransmitter receptor

Query Match 15.5%; Score 758; DB 2; Length 915;

Best Local Similarity 24.3%; Pred. No. 2.4e-47;

Matches 214; Conservative 191; Mismatches 354; Indels 120; Gaps 32;

QY 53 LVIGGLFPIDSRITIPANESILEPASAKCEGFNFQR-FRWMKAMIHMIKEINKRKDILPNI 111

Db 49 VTLGGLFPVHAK-----GPSGVPCGDIKRENGIHRLEAMLYALDQINSDPNLLPNV 99

QY 112 TLGYQIFDTCFTTISKVSVEAVLVLGTGQ-EENRPNFRNSTGAFP-----AGIVGAGGS 162

Db 100 TLGARILDTCSDRTYALEQSLTFVQALIQDTSVRCCTNGEPFVFKPEKVGVIGASGS 159

QY 163 FLSVPASRILGLYLPQVGYTSTCVILSDKYQFPSPYLRLVIASDKIQSKAVVKRIQHFQW 222

Db 160 SVSIVMANILRFQIPQISYASTAPELSDRRYDFFSRVPPDSFOAQAMVDIVKALGN 219

QY 223 WYGAIAADDDYGYGVKTFKE-KMESANLCVAFSETIPKVYSNEKMQKAV-----KAV 274

Db 220 YVSTLASEGSYGEKGVESFTQISKEAGGLCIAQSVRIPQ---ERKDRITDFDRIIKQLL 275

QY 275 KTSTAKVIVLYTSDIDLFLV-----LEMIHNNITDRTWIATEAWITSALIAKPEYFPYF 329

Db 276 DTENSRAVVIFANDEDIKQILAAAKRADQVGHFL---WVGSDSW-GSKINPLHQHEDIA 330

QY 330 GGTIGFATPRSVIPGLKFLYDVHPNKPDPNDVLTIEFWQTAFNCTWPNSSVPYNVDHRVN 389

Db 331 EGAITIQPKRATVEGFDAYFTSRTLNNRRNVFAEYWEENFNC-----KLT 377

QY 390 MTG--KEDRLYDMSDQLCTGEEKLEDLKNYTLDTSQLRITKQCKQAVYAIAGLDHLR- 446

Db 378 IGSKKED----TDRKCTGQERIGKDSN-YEQBGKVQFV---IDAVYAMAHALHHMNKD 428

QY 447 -CQEGQGPFGSNQQCAIYPTFDWQLMYVMKEIKFKSHEDKWILDDNGDLKNGHYDVLN 505

Db 429 LCADYRG-----VCPENEQAGGKLLKYIRHVNFNNGSAGTPVMFNKNGDAP-GRYDIFQ 481

QY 506 WHLDDEGEISFVTVGRFNFRSTNFELVIPTNSTIFWNTESSRLPHSVCTDVCPPGTGRGF 565

Db 482 YQTTNTTNPYRLIGQW---TDELQJNI---EDMQWKGKGVREIPSSVCTLPCKPGQ-RKK 534

QY 566 VQREPICCFDSIPCADGHVSRKPGERECEQCCEGYWSNAQKSECVLKEVEYLAYDEALGF 625

Db 535 TQKGTGCCWTCEPC-DGY-QYQFDEMTQCHCPYDQRNENRTGCQNIPPIKLEWHPWAV 592

QY 626 TLVILSVFGAFVVLAVTAVVVIHRHTPLVNASDWQLGFLIQVSLIIMLLSSMLFIDKPHN 685

Db 593 IPVFLAMLGIIATIFVMATFIRYNDTPIVRASGRELSVLLTGIFLCYIITFLMIKPDV 652

QY 686 WSCMAGQVTLALGFSLCLSGTSSFLAYRI-SKSKTQLTSMHPLYRKIIIVLISVLA 744

Db 653 AVCSFRRVFLGLGMCISYAALLTKTNRI---YRIFEQKKSVTAPR-----LISPTS 701

QY 745 EIGICTAYLI-----LEPPMV-----YKNMESQNTKIILGCNEISIEFLYSM 786

Db 702 QLAI-TSSLISVQLLGVFIWFGVDPNIIIDYDEHKTNPQARGVLKCDITDLQIICSL 760

QY 787 FGIDAFLLALLCFLTTFVARQLPDNYEGKCITFGMLVFFIIMWSFVPVYLST-KGKFKMA 845

Db 761 -GYSILLMVTCTVYAIKTRGVPENFNEAKPIGFTMYTTCIIVWLAFIPIFFGTAQSAEKLY 819

QY 846 VE---IFAILASSHGLLGCIFAPKCLIIILLRPERNTSE 880

Db 820 IQTTTLTISMNLSASVALGMLYMPKVYIIIFHPELNVQK 858

RESULT 15

A46742

metabotropic glutamate receptor, mGluR6 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004

C;Accession: A46742

R;Nakajima, Y.; Iwakabe, H.; Akazawa, C.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, J. Biol. Chem. 268, 11868-11873, 1993

A;Title: Molecular characterization of a novel retinal metabotropic glutamate receptor m

A;Reference number: A46742; MUID:93280152; PMID:8389366

A;Accession: A46742

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-871 <NAK>

A;Cross-references: UNIPROT:P35349; GB:D13963; NID:G391856; PIDN:BAA03066.1; PID:G391857

A;Experimental source: retina

A;Note: sequence extracted from NCBI backbone (NCBIN:133246, NCBIIP:133250)

C;Superfamily: metabotropic glutamate receptor 4

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 14.8%; Score 724.5; DB 2; Length 871;

Best Local Similarity 24.9%; Pred. No. 6.4e-45;

Matches 217; Conservative 174; Mismatches 380; Indels 101; Gaps 28;

QY 53 LVIGGLFPIDSRITIPANESILEPASAKCEGF-NFQFRWMKAMIHMIKEINKRKDILPNI 111

Db 33 LTLGGLFPVHAR-----GAAGRACGALKKEQGVHRLEAMLYALDRVNADPELLPGV 83

QY 112 TLGYQIFDTCFTTISKVSVEAVLVLGTQEENR-----PNFRNSTGAFPAIV 157

Db 84 RLGARLLDTCSDRTYALEQALSFVQALIRGRGDGEASVRCPGVPLRSAPPERWAVV 143

QY 158 GAGGSFLSVPASRILGLYLPQVGYTSTCVILSDKYQFPSPYLRLVIASDKIQSKAVVKRIQ 217

Db 144 GASASSVSIMVANVLRLEFAIPQISYASTAPELSDSTRYDFFSRVPPDSYQAQAMVDIVR 203

QY 218 HFGWVWVGAIADDDYGYGVKTFKE-KMESANLCVAFSETIPKVYSNEKMQKAV-KAVK 275

Db 204 ALGWNVYSTLASEGNYGESGVFAFVQISREAGGVCIQAQSIKIPREPKPGEFHKVIRRLME 263

QY 276 TSFAKVIVLYTSDIDLFLVLEMIHNNITDR-TWIAATEAW---ITSALIAKPEYFPYFGG 331

Db 264 TPNARGIIFIANEDDIRRVLEATFRQANLTGHFLWVGSDSWGSKIIPILNLEEAV----G 319





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